



ANTIBODIES DIRECTED TO PDGFD AND USES THEREOF  
*Corvalan et al.*  
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FIGURE 23

Figure 23A

	Section 1					
	(1) 1	10	20	30	40	51
CUR2-1.6.1 HC	(1) EVQLVSEGGLVKGPGSLRLSCAASGF	Y	N	M	W	VQAPGKGLE
VH3-21	(1) EVQLVSEGGLVKGPGSLRLSCAASGETF	S	Y	M	N	VQAPGKGLE
Consensus	(1) EVQLVSEGGLVKGPGSLRLSCAASGF	P	Y	M	W	VQAPGKGLE
	Section 2					
	(52) 52	60	70	80	90	102
CUR2-1.6.1 HC	(52) SSSSSNIVYYADSVKGRFTISRDNAKNSLYQMN	S	T	R	A	E
VH3-21	(52) SSSSSYIYYADSVKGRFTISRDNAKNSLYQMN	S	T	R	A	E
Consensus	(52) SSSSS IYYADSVKGRFTISRDNAKNSLYQMN	S	T	R	A	E
	Section 3					
	(103) 103	110	126			
CUR2-1.6.1 HC	(103) TFGGIIASFYFDYWGQGT	L	V	T	V	S
VH3-21	(99) -----	-----	-----	-----	-----	-----
Consensus	(103)					

Figure 23B

	Section 1					
	(1) 1	10	20	30	40	51
CUR2-1.6.1 LC	(1) DIQMTQSPSLSA9VGDRVTITCRASQGIRNDLGW	Q	Q	K	P	G
A30	(1) DIQMTQSPSLSA9VGDRVTITCRASQGIRNDLGW	Q	Q	K	P	G
Consensus	(1) DIQMTQSPSLSA9VGDRVTITCRASQGIRNDLGW	Q	Q	K	P	G
	Section 2					
	(52) 52	60	70	80	90	102
CUR2-1.6.1 LC	(52) SSIQSGVP8RF3G3GGCTEFTLTIS	S	L	Q	P	E
A30	(52) SSIQSGVP8RF3G3GGCTEFTLTIS	S	L	Q	P	E
Consensus	(52) SSIQSGVP8RF3G3GGCTEFTLTIS	S	L	Q	P	E
	Section 3					
	(103) 103	107				
CUR2-1.6.1 LC	(103) KVEIK	SEQ ID NO:14				
A30	(96) -----	SEQ ID NO:11				
Consensus	(103)					



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**FIGURE 24**

Figure 24A

										Section 1
	(1)	1	10	20	30	40				51
Cur2-1.11.1	HC	(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNNMSWVRQAPGKGLEWVSVI							
VH3-53		(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNNMSWVRQAPGKGLEWVSVI							
Consensus		(1)	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNNMSWVRQAPGKGLEWVSVI							
										Section 2
	(52)	52	60	70	80	90				102
Cur2-1.11.1	HC	(52)	YSGGSTYYADSVKGRFTISRDNSKNTLYLQMNNSLPAEDTAVYYCAGTVTTN							
VH3-53		(52)	YSGGSTYYADSVKGRFTISRDNSKNTLYLQMNNSLPAEDTAVYYCAR-----							
Consensus		(52)	YSGGSTYYADSVKGRFTISRDNSKNTLYLQMNNSLRAEDTAVYYCA							
										Section 3
	(103)	103	110	120						
Cur2-1.11.1	HC	(103)	YYGGMDVWGQGTTVTVSS	SEQ ID NO:15						
VH3-53		(98)	-----	SEQ ID NO:5						
Consensus		(103)	-----							

Figure 24B



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**FIGURE 25**

**Figure 25A**

	Section 1				
	10	20	30	40	51
CR2-1.17.1_HC	(1) QVQLVE <del>SGGGVVQPG</del> SIRLS <del>CAASGPTFSSYGMH</del> WVR <del>OAPGK</del> GLEWVAVI				
VH3-33	(1) QVOLVE <del>SGGGVVQPG</del> SIRLS <del>CAASGETSSYGMH</del> NVR <del>OAPGK</del> GLEWVAVI				
Consensus	(1) QVQLVE <del>SGGGVVQPG</del> SIRLS <del>CAASGPTFSSYGMH</del> WVR <del>OAPGK</del> GLEWVAVI				
	Section 2				
	52	60	70	80	90
CR2-1.17.1_HC	(52) WYDGSN <del>KYYADSVK</del> GRFTISRDNSKNTLYLQMNSLRAEDTAVYYC <del>ARDQ</del> GY				102
VH3-33	(52) WYDGSN <del>KYYADSVK</del> GRFTISRDNSKNTLYLQMNSLRAEDTAVYYC <del>AR</del> ---				
Consensus	(52) WYDGSN <del>KYYADSVK</del> GRFTISRDNSKNTLYLQMNSLRAEDTAVYYC <del>AR</del>				
	Section 3				
	103	110	126		
CR2-1.17.1_HC	(103) RYAG <del>YDYGMDVNGQGTTV</del> S SEQ ID NO:17				
VH3-33	(99) ----- SEQ ID NO:4				
Consensus	(103)				

**Figure 25B**

	Section 1				
	10	20	30	40	52
CR2-1.17.1_LC	(1) DIQMTQSP <del>SLSASV</del> GDRVTITC <del>RASQG</del> IRNDL <del>IGWYQQ</del> K <del>PGK</del> A <del>PKR</del> L <del>IY</del> A <del>S</del>				
A30	(1) DIQMTQSP <del>SLSASV</del> GDRVTITC <del>RASQG</del> IRNDL <del>IGWYQQ</del> K <del>PGK</del> A <del>PKR</del> L <del>IY</del> A <del>S</del>				
Consensus	(1) DIQMTQSP <del>SLSASV</del> GDRVTITC <del>RASQG</del> IRNDL <del>IGWYQQ</del> K <del>PGK</del> A <del>PKR</del> L <del>IY</del> A <del>S</del>				
	Section 2				
	53	60	70	80	90
CR2-1.17.1_LC	(53) S <del>LG</del> SGVP <del>SRFSGSGSG</del> T <del>EFTLT</del> IS <del>LQ</del> P <del>EDF</del> AT <del>YYC</del> Q <del>HNS</del> S <del>YP</del> L <del>T</del> P <del>GGG</del> T <del>KV</del>				104
A30	(53) S <del>LG</del> SGVP <del>SRFSGSGSG</del> T <del>EFTLT</del> IS <del>LQ</del> P <del>EDF</del> AT <del>YYC</del> Q <del>HNS</del> S <del>YP</del> -----				
Consensus	(53) S <del>LG</del> SGVP <del>SRFSGSGSG</del> T <del>EFTLT</del> IS <del>LQ</del> P <del>EDF</del> AT <del>YYC</del> Q <del>HNS</del> S <del>YP</del>				
	Section 3				
CR2-1.17.1_LC	(105) 1087 EIK SEQ ID NO:18				
A30	(96) --- SEQ ID NO:11				
Consensus	(105)				



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**FIGURE 26**

**Figure 26A**

						Section 1
	(1) 1	10	20	30	40	52
CR2-1.18_HC	(1) QVQLVQSGAEVIRKPGASVVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMN					
VH1-8	(1) QVQLVQSGAEVKKPGASVVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMN					
Consensus	(1) QVQLVQSGAEVKKPGASVVKVSKASGYTFTSYDINWVRQATGQGLEWMGWMN					
						Section 2
	(53) 53	60	70	80	90	104
CR2-1.18_HC	(53) PN8GNTGYAQRKFQGRVTMTRNTS	-----	-----	-----	-----	
VH1-8	(53) PN8GNTGYAQRKFQGRVTMTRNTS	-----	-----	-----	-----	
Consensus	(53) PN8GNTGYAQRKFQGRVTMTRNTS	-----	-----	-----	-----	
						Section 3
	(105) 105	110	126			
CR2-1.18_HC	(105) GTYYYYYYGMDVWGQGTTVTVSS			SEQ ID NO:19		
VH1-8	(99) -----			SEQ ID NO:1		
Consensus	(105)					

**Figure 26B**

						Section 1
	(1) 1	10	20	30	40	53
CR2-1.18_LC	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQREGRAEKRLLIYAASS					
A30	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKEGKAEKRLLIYAASS					
Consensus	(1) DIQMTQSPSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLLIYAASS					
						Section 2
	(54) 54	60	70	80	90	106
CR2-1.18_LC	(54) DQSGVPSRPSGSGSGTETFTLTISLQPEDPATY	-----	-----	-----	-----	
A30	(54) DQSGVPSRPSGSGSGTETFTLTISLQPEDPATY	-----	-----	-----	-----	
Consensus	(54) DQSGVPSRPSGSGSGTETFTLTISLQPEDPATY	-----	-----	-----	-----	
						Section 3
	(107) 107					
CR2-1.18_LC	(107) K	SEQ ID NO:20				
A30	(96) -	SEQ ID NO:11				
Consensus	(107)					



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**FIGURE 27**

**Figure 27A**

	Section 1					
	1	10	20	30	40	52
Cur2-1.19.1_hc	(1) QVOLVQSGAEVKKPGASVKVSCKA SGYTFPSYDINWVRQATGQGLEWMGWMN					
VH1-8	(1) QVOLVQSGAEVKKPGASVKVSCKA SGYTFPSYDINWVRQATGQGLEWMGWMN					
Consensus	(1) QVOLVQSGAEVKKPGASVKVSCKA SGYTFPSYDINWVRQATGQGLEWMGWMN					
	Section 2					
	(53) 53	60	70	80	90	104
Cur2-1.19.1_hc	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSLRSEDTAVYYCARDVMITP					
VH1-8	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSLRSEDTAVYYCAR-----					
Consensus	(53) PNSGNTGYAQKFQGRVTMTRNTSISTAYMELSLRSEDTAVYYCAR					
	Section 3					
	(105) 105	110	126			
Cur2-1.19.1_hc	(105) GGIVIVHYGMDVWQGTTTVSS			SEQ ID NO:21		
VH1-8	(99) -----			SEQ ID NO:1		
Consensus	(105)					

**Figure 27B**

	Section 1					
	1	10	20	30	40	52
Cur2-1.19.1_lc	(1) DIQMTQSPSSLSAVGDRVTITCRA SGQIRNDLGWYQQKPGKAPKRILYAA					
A30	(1) DIQMTQSPSSLSAVGDRVTITCRA SGQIRNDLGWYQQKPGKAPKRILYAA					
Consensus	(1) DIQMTQSPSSLSAVGDRVTITCRA SGQIRNDLGWYQQKPGKAPKRILYAA					
	Section 2					
	(53) 53	60	70	80	90	104
Cur2-1.19.1_lc	(53) SLOSGGVPSRFSGSGSGTFTLTISLOPEDFATYYCLQHNSDPCSFQGQTKL					
A30	(53) SLOSGGVPSRFSGSGSGTFTLTISLOPEDFATYYCLQHNSDPCSFQGQTKL					
Consensus	(53) SLOSGGVPSRFSGSGSGTDFLTISLOPEDFATYYCLQHNSDPCSFQGQTKL					
	Section 3					
	(105) 1067					
Cur2-1.19.1_lc	(105) EIR		SEQ ID NO:22			
A30	(96) ---		SEQ ID NO:11			
Consensus	(105)					



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**FIGURE 28**

**Figure 28A**

	Section 1					
	1	10	20	30	40	51
Cur2-1.23.1_HC	(1)					
VH5-51	(1)	EVOLVOSGABVKRPGESLKIISCEGSGVSYTSYWIGWVRQMPGKGLEWMGII				
Consensus	(1)	EVQLVQSGAEVKKPGESLKIISCGSYTSYWIGWVRQMPGKGLEWMGII				
	Section 2					
	52	60	70	80	90	102
Cur2-1.23.1_HC	(52)	YPGDSDTRYSPSPQQVTISADKSISTAYLQWSSLKASDTAMYYCARHVSY				
VH5-51	(52)	YPGDSDTRYSPSPQQVTISADKSISTAYLQWSSLKASDTAMYYCAR-----				
Consensus	(52)	YPGDSDTRYSPSPQQVTISADKSISTAYLQWSSLKASDTAMYYCAR				
	Section 3					
	103	110	126			
Cur2-1.23.1_HC	(103)	YYV8G8YYNVFDYWGQGTIVTVSS			SEQ ID NO:23	
VH5-51	(99)	-----			SEQ ID NO:6	
Consensus	(103)					

**Figure 28B**

	Section 1					
	1	10	20	30	40	51
Cur2-1.23.1_LC	(1)					
A30	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQIPEGKAPKRKLIYAA				
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQIPEGKAPKRKLIYAA				
	Section 2					
	52	60	70	80	90	102
Cur2-1.23.1_LC	(52)	SSIQORGVPSPRF3GEGSGTEFTLTISSLQPEDFATYYCLQHNSYEWTFGQGT				
A30	(52)	SSIQORGVPSPRF3GEGSGTEFTLTISSLQPEDFATYYCLQHNSYEWTFGQGT-----				
Consensus	(52)	SSIQORGVPSPRF3GEGSGTEFTLTISSLQPEDFATYYCLQHNSYEWTFGQGT				
	Section 3					
	103	107				
Cur2-1.23.1_LC	(103)	KVEIK	SEQ ID NO:24			
A30	(96)	-----	SEQ ID NO:11			
Consensus	(103)					



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**FIGURE 29**

**Figure 29A**

	1	10	20	30	40	51	Section 1
CR2-1.24.1 HC	(1)	QVQLVESGGGVQPGRSRLSCAASGF	FSSYGMHWVRQAPGKGLEWVADI				
VH3-33	(1)	QVQLVESGGGVQPGRSRLSCAASGF	FSSYGMHWVRQAPGKGLEWVAVI				
Consensus	(1)	QVQLVESGGGVQPGRSRLSCAASGF	FSSYGMHWVRQAPGKGLEWVA I				
	52	60	70	80	90	102	Section 2
CR2-1.24.1 HC	(52)	WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARQGY					
VH3-33	(52)	WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR---					
Consensus	(52)	WYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR					
	103	110	126				Section 3
CR2-1.24.1 HC	(103)	SYGYVYYDYGMDVWGQGTTVTVSS	SEQ ID NO:25				
VH3-33	(99)	-----	SEQ ID NO:4				
Consensus	(103)	-----					

**Figure 29B**

	1	10	20	30	40	52	Section 1
CR2-1.24.1 LC	(1)	DIQMTQSPSBSAASVGDRVITITCRASQGIRNDLGWYQQKEGKAKPRRLIYAAAS					
A30	(1)	DIQMTQSPSBSAASVGDRVITITCRASQGIRNDLGWYQQKEGKAKPRRLIYAAAS					
Consensus	(1)	DIQMTQSPSBSAASVGDRVITITCRASQGIRNDLGWYQQKEGKAKPRRLIYAAAS					
	53	60	70	80	90	104	Section 2
CR2-1.24.1 LC	(53)	SLQSGVPSRFSGSGSGTEFTLTISILOPEDPATYYCLOHNSYPWTFGQGTV					
A30	(53)	SLQSGVPSRFSGSGSGTEFTLTISILOPEDPATYYCLOHNSYP-----					
Consensus	(53)	SLQSGVPSRFSGSGSGTEFTLTISILOPEDPATYYCLOHNSYP					
	105	1067					Section 3
CR2-1.24.1 LC	(105)	EIK	SEQ ID NO:26				
A30	(96)	---	SEQ ID NO:11				
Consensus	(105)	-----					



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**FIGURE 30**

**Figure 30A**

	Section 1					
	1	10	20	30	40	51
VH5-51	(1) EVQLVQSGAEVKKPGESLKIISCKGSGYFTSYWIGWVRQMPGKGLEWMGII					
CR2-1.25.1_HC	(1) EVQLVQSGAEVKKPGESLKIISCKGSGYFTSYWIGWVRQMPGKGLEWMGII					
Consensus	(1) EVQLVQSGAEVKKPGESLKIISCKGSGYFTSYWIGWVRQMPGKGLEWMGII					
	Section 2					
	52	60	70	80	90	102
VH5-51	(52) YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR					
CR2-1.25.1_HC	(52) YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR					
Consensus	(52) YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR					
	Section 3					
	103	110	126			
VH5-51	(99) YYGSETYYNVFDYWGQGTLTVSS			SEQ ID NO:6		
CR2-1.25.1_HC	(103) YYGSETYYNVFDYWGQGTLTVSS			SEQ ID NO:27		
Consensus	(103)					

**Figure 30B**

	Section 1					
	1	10	20	30	40	52
A30	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKEGRKPLRILYAA					
CR2-1.25.1_LC	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKEGRKPLRILYAA					
Consensus	(1) DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKEGRKPLRILYAA					
	Section 2					
	53	60	70	80	90	104
A30	(53) SLQSGVPSRFSGSGSGTEFTLTISISSLQPEDFATYYCLQHNSYP					
CR2-1.25.1_LC	(53) SLQSGVPSRFSGSGSGTEFTLTISISSLQPEDFATYYCLQHNSYP					
Consensus	(53) SLQSGVPSRFSGSGSGTEFTLTISISSLQPEDFATYYCLQHNSYP					
	Section 3					
	105	108				
A30	(96) EIK	SEQ ID NO:11				
CR2-1.25.1_LC	(105) EIK	SEQ ID NO:28				
Consensus	(105)					



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**FIGURE 31**

**Figure 31A**

	Section 1					
VH5-51	(1) 1	10	20	30	40	52
CR2-1.29_HC	(1) EVQLVQSGAEVKRPGE3LK13CKGSGY8FTSYWIGWVRQMPGRGLEWMGIY					
Consensus	(1) EVQLVQSGAEVKRPGE3LK13CKGSGY8FTSYWIGWVRQMPGRGLEWMGIY					
	Section 2					
VH5-51	(53) 53	60	70	80	90	104
CR2-1.29_HC	(53) PGDSDTRYSPSFQGQATISADKSISTAYLQWSSLRASDTAMYYCAR-----					
Consensus	(53) PGDSDTRYSPSFQGQATISADKSISTAYLQWSSLRASDTAMYYCARHVDVGA					
	Section 3					
VH5-51	(105) 105	110	129			
CR2-1.29_HC	(105) TIGGYYYYYHGMDVWGQGTTVTVSS			SEQ ID NO:6		
Consensus	(105)			SEQ ID NO:29		

**Figure 31B**

	Section 1					
A19	(1) 1	10	20	30	40	53
CR2-1.29_LC	(1) DIVMTQSPLSLPVTPGEPAISCRSSQSLLHSNGNYLDWYLQKPGQSPQLLI					
Consensus	(1) DIVMTQSPLSLPVTPGEPAISCRSSQSLLHSNGNYLDWYLQKPGQSPQLLI					
	Section 2					
A19	(54) 54	60	70	80	90	106
CR2-1.29_LC	(54) YLGSNRASGVPDFSGSGSGTDFTLKISRVEA[DVGVYYCMQALQS]P-----					
Consensus	(54) YLGSNRASGVPDFSGSGSGTDFTLKISRVEA[DVGVYYCMQALQS]LMCSFGQ					
	Section 3					
A19	(107) 107	113				
CR2-1.29_LC	(107) GTKLEIK			SEQ ID NO:8		
Consensus	(107)			SEQ ID NO:30		



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**FIGURE 32**

**Figure 32A**

	Section 1				
	10	20	30	40	52
VH1-18	(1) 1				
CR2-1.33_HC	(1) QVQLVQSGAEVKPGASVKVSKCASGYTFTSYGISMVRQAEQGQGLEWMGWIS				
Consensus	(1) QVQLVQSGAEVKPGASVKVSKCASGYTFTSYGISMVRQAFPGQGLEWMGWIS				
					Section 2
	53	60	70	80	90
VH1-18	(53) AYNGNTNYAQLQGRVTMTTDTSTSTAYMELRSRLRSDDTAVYYCAR-----				104
CR2-1.33_HC	(53) AYNGNTNYAQLQGRVTMTTDTSTSTAYMELRSRLRSDDTAVYYCARDHYYDS				
Consensus	(53) AYNGNTNYAQLQGRVTMTTDTSTSTAYMELRSRLRSDDTAVYYCAR				
					Section 3
	(105) 105	110	127		
VH1-18	(99) -----				
CR2-1.33_HC	(105) SDYLYYYYGLDVWQGQTTTVSS			SEQ ID NO:2	
Consensus	(105)			SEQ ID NO:31	

**Figure 32B**

	Section 1				
	10	20	30	40	53
A20	(1) 1				
CR2-1.33_LC	(1) DIQMTQSPSS1SASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAAST				
Consensus	(1) DIQMTQSPSS1SASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAAST				
					Section 2
	54	60	70	80	90
A20	(54) I0SGGVESRESGBGSQTDFTLTISILOPEDVATYYCQKYN5AP-----				106
CR2-1.33_LC	(54) I0SGGVESRESGBGSQTDFTLTISILOPEDVATYYCQKYN5AP				
Consensus	(54) I0SGGVESRESGBGSQTDFTLTISILOPEDVATYYCQKYN5AP				
					Section 3
	(107) P07				
A20	(96) -		SEQ ID NO:9		
CR2-1.33_LC	(107) K		SEQ ID NO:32		
Consensus	(107)				



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**FIGURE 33**

**Figure 33A**

	Section 1					
	(1) 1	10	20	30	40	51
VH3-33	(1) QVOLVESGGGVVQPGRSRLSCAASGFTFSSYGMHHWVRQAPGKGLEWVAII					
CR2-1.38.1_HC	(1) QVOLVESGGGVVQEGRSRLSCAASGFTFSSYGMHHWVRQAPGKGLEWVAII					
Consensus	(1) QVOLVESGGGVVQPGRSRLSCAASGFTFSSYGMHHWVRQAPGKGLEWVAII					
	Section 2					
	(52) 52	60	70	80	90	102
VH3-33	(52) WYDGGSNKYYADSVKGRFTI9RDNSKNTLYLQMN9LRAEDTAVYYCAR---					
CR2-1.38.1_HC	(52) WYDGNDKYYADSVKGRFTI9RDNSKNTLYLQMN9LRAENTI9YYCARGYYY					
Consensus	(52) WYDG KYYADSVKGRFTI9RDNSKNTLYLQMN9LRAEDTAVYYCAR					
	Section 3					
	(103) 103	110	127			
VH3-33	(99) -----			SEQ ID NO:4		
CR2-1.38.1_HC	(103) DSSDYLYYYYGMDVWGQGTTVTVSS			SEQ ID NO:33		
Consensus	(103)					

**Figure 33B**

	Section 1					
	(1) 1	10	20	30	40	52
A20	(1) DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAAS					
CR2-1.38.1_LC	(1) DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAAS					
Consensus	(1) DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAAS					
	Section 2					
	(53) 53	60	70	80	90	104
A20	(53) TLQSGVPSRF3GSGSGTDFSLTISIQLQPEDVATYYCQKCN9APWTFGQGTTV					
CR2-1.38.1_LC	(53) TLQSGVPSRF3GSGSGTDFSLTISIQLQPEDVATYYCQKCN9APWTFGQGTTV					
Consensus	(53) TLQSGVPSRF3GSGSGTDFSLTISIQLQPEDVATYYCQKCN9APWTFGQGTTV					
	Section 3					
	(105) 105					
A20	(96) ---			SEQ ID NO:9		
CR2-1.38.1_LC	(105) EIK			SEQ ID NO:34		
Consensus	(105)					



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FIGURE 34

Figure 34A

	Section 1				
	(1) 1	10	20	30	40
VH5-51	(1) EVQLVQSGAEVKKPGEGLKISCKGSGYSPFTSYWIGWVRQMPGKGLEWMGII				51
CR2-1.39.1_HC	(1) EVQLVQSGTEVKPGEGLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGII				
Consensus	(1) EVQLVQSG EVKKPGEGLKISCKGSGY PTSYWIGWVRQMPGKGLEWMGII				
	Section 2				
	(52) 52	60	70	80	90
VH5-51	(52) YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR-----				102
CR2-1.39.1_HC	(52) YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR-----				
Consensus	(52) YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR-----				
	Section 3				
	(103) 103	110	126		
VH5-51	(99) -----			SEQ ID NO:6	
CR2-1.39.1_HC	(103) YYNSGSYYNVFDYWGQGTIVTVSS			SEQ ID NO:35	
Consensus	(103)				

Figure 34B

	Section 1				
	(1) 1	10	20	30	40
A30	(1) DIQMTQSPSSLSASVGDRVITTCRASQGIRNDLGWYQQKEGKAPKRLIYAA3				52
CR2-1.39.1_LC	(1) DIQMTQSPSSLSASVGDRVITTCRASQGIRNDLGWYQQKEGKAPKRLIYAA3				
Consensus	(1) DIQMTQSPSSLSASVGDRVITTCRASQGIRNDLGWYQQKEGKAPKRLIYAA3				
	Section 2				
	(53) 53	60	70	80	90
A30	(53) SLOSGVPSRFSGSGSGTEFTLTISLOPEDFATYYC1QHNSYP-----				104
CR2-1.39.1_LC	(53) SLOSGVPSRFSGSGSGTEFTLTISLOPEDFATYYC1QHNSYPWTFGQGTKV				
Consensus	(53) SLOSGVPSRFSGSGSGTEFTLTISLOPEDFATYYC1QHNSYP				
	Section 3				
	(105) 1007				
A30	(96) ---			SEQ ID NO:11	
CR2-1.39.1_LC	(105) EIK			SEQ ID NO:36	
Consensus	(105)				



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FIGURE 35

Figure 35A

										Section 1
	(1)	1	10	20	30	40	50	52		
VH1-8	(1)	QVOLVQSGAEVKRPGAVKVSCKASGYTFSYDINWVRQATGQGLEWMGWMN								
CR2-1.45_HC	(1)	QVQLVQSGAEVKRPGAVKVSCKASGYTFSYDINWVRQATGQGLEWMGWMN								
Consensus	(1)	QVQLVQSGAEVKRPGAVKVSCKASGYTFSYDINWVRQATGQGLEWMGWMN								
										Section 2
	(53)	53	60	70	80	90	100	104		
VH1-8	(53)	PNSGNTGYAQQKFOGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR								
CR2-1.45_HC	(53)	PNSGNTGYAQQKFOGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR								
Consensus	(53)	PNSGNTGYAQQKFOGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR								
										Section 3
	(105)	105	110	125						
VH1-8	(99)	-----								
CR2-1.45_HC	(105)	GYDYYYYGMDVWGQGTTTVSS								
Consensus	(105)	-----								
									SEQ ID NO:1	
									SEQ ID NO:38	

Figure 35B

										Section 1
	(1)	1	10	20	30	40	50	53		
A20	(1)	DIQMTQSPSSILASAVGDRVTITCRASQGISNYLAWYQQKPGKVKLLIYAAST								
CR2-1.45_LC	(1)	DIQMTQSPSSILASAVGDRVTITCRASQGISNDLAWYQQKPGKVKLLIYAAST								
Consensus	(1)	DIQMTQSPSSILASAVGDRVTI CRASQGISM LAWYQQKPGKVKLLIYAAST								
										Section 2
	(54)	54	60	70	80	90	100	106		
A20	(54)	DQSGVFSRSGSGSGTDTITLISIOPEDVATYYCQKYN3AP								
CR2-1.45_LC	(54)	DQSGVFSRSGSGSGTDTITLISIOPEDVATYYCQKYN3APFTFGPGTKVDI								
Consensus	(54)	DQSGVFSRSGSGSGTDTITLISIOPEDVATYYCQKYN3APFTFGPGTKVDI								
										Section 3
	(107)	107								
A20	(96)	-								
CR2-1.45_LC	(107)	K								
Consensus	(107)	K								
									SEQ ID NO:9	
									SEQ ID NO:39	



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FIGURE 36

Figure 36A

	1	10	20	30	40	51	Section 1
VH1-8	(1) QVQLVQSGAEVKKPGASVVKVSKASGY						
CR2-1.46.1_HC	(1) QVQLVQSGAEVKKPGASVVKVSKASGY						
Consensus	(1) QVQLVQSGAEVKKPGASVVKVSKASGY						
							Section 2
VH1-8	(52) 52	60	70	80	90	102	
CR2-1.46.1_HC	(52) NPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR						
Consensus	(52) NPNNNGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCAR						
							Section 3
VH1-8	(103) 103	110		126			
CR2-1.46.1_HC	(99) VVTATDYYGGMDVWGQGTTTVSS				SEQ ID NO:1		
Consensus	(103)				SEQ ID NO:40		

Figure 36B

	1	10	20	30	40	52	Section 1
A30	(1) DIQMTQSPSSISASVGDRTITCRASQGIRNDLGWYQQKEPGKAPKRLLPAAAS						
CR2-1.46.1_LC	(1) DIQMTQSPSSISASVGDRTITCRASQGIRNDLGWYQQKEPGKAPKRLLPAAAS						
Consensus	(1) DIQMTQSPSSISASVGDRTITCRASQGIRNDLGWYQQKEPGKAPKRLLPAAAS						
							Section 2
A30	(53) 53	60	70	80	90	104	
CR2-1.46.1_LC	(53) S1QSGVPSRF2G3G3GTEFTLTISIISIOPEDPATYYCLQH3GYPPPTFGQGTV						
Consensus	(53) S1QSGVPSRF2G3G3GTEFTLTISIISIOPEDPATYYCLQH3GYPPPTFGQGTV						
							Section 3
A30	(105) 105						
CR2-1.46.1_LC	(96) EIK				SEQ ID NO:11		
Consensus	(105)				SEQ ID NO:41		



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FIGURE 37

Figure 37A

						Section 1
	1	10	20	30	40	51
CR2-1.48.1_HC	(1)	QVQLVQSGAEVKKPQASVKVSKRASGYTFTSYGIVSWVRQAPGQGLEWMGWI				
VH1-18	(1)	QVQLVQSGAEVKKPQASVKVSKRASGYTFTSYGIVSWVRQAPGQGLEWMGWI				
Consensus	(1)	QVQLVQSGAEVKKPQASVKVSKRASGYTFTSYGIVSWVRQAPGQGLEWMGWI				
						Section 2
	52	60	70	80	90	102
CR2-1.48.1_HC	(52)	SAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCARVEY				
VH1-18	(52)	SAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCAR---				
Consensus	(52)	SAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLSRSDDTAVYYCAR				
						Section 3
	103	110	125			
CR2-1.48.1_HC	(103)	YYDGSGYYYFDYWGQGTIVTVSS	SEQ ID NO:42			
VH1-18	(99)	-----	SEQ ID NO:2			
Consensus	(103)					

Figure 37B

						Section 1
	1	10	20	30	40	52
CR2-1.48.1_LC	(1)	DIQMTQSPSSVSASVGDRVITITCRASQGISESWLAWYQQKPGKAPKLLIYAA				
L5	(1)	DIQMTQSPSSVSASVGDRVITITCRASQGISESWLAWYQQKPGKAPKLLIYAA				
Consensus	(1)	DIQMTQSPSSVSASVGDRVITITCRASQGISESWLAWYQQKPGKAPKLLIYAA				
						Section 2
	53	60	70	80	90	104
CR2-1.48.1_LC	(53)	IIQSGVPSRFSGSGSGTDFTLTISLQPEDFAYYCCQNSFPRTFGQGTKV				
L5	(53)	SIQSGVPSRFSGSGSGTDFTLTISLQPEDFAYYCCQNSFP-----				
Consensus	(53)	IQSGVPSRFSGSGSGTDFTLTISLQPEDFAYYCCQNSFP				
						Section 3
	105	1087				
CR2-1.48.1_LC	(105)	EIK	SEQ ID NO:43			
L5	(96)	---	SEQ ID NO:7			
Consensus	(105)					



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**FIGURE 38**

**Figure 38A**

	Section 1					
	1	10	20	30	40	51
CR2-1.49.1_HC	(1)	QVOLVQSGAEVKKPGASVVKVSCKASGYTFTSYDINWWROATGOQGLEWMGWM				
VH1-8	(1)	QVOLVQSGAEVKKPGASVVKVSCKASGYTFTSYDINWWROATGOQGLEWMGWM				
Consensus	(1)	QVOLVQSGAEVKKPGASVVKVSCKASGYTFTSYDINWWROATGOQGLEWMGWM				
	Section 2					
	52	60	70	80	90	102
CR2-1.49.1_HC	(52)	NPNSGDTGYAQKFOGRVTMTPNTSISTAYMELSSLRSEDTAVYFCARMRDI				
VH1-8	(52)	NPNSGNTGYAQKFOGRVTMTRNTSISTAYMELSSLRSEDTAVYFCAR---				
Consensus	(52)	NPNSG TGYAQKFOGRVTMTRNTSISTAYMELSSLRSEDTAVYFCAR				
	Section 3					
	103	110	110	127		
CR2-1.49.1_HC	(103)	VATSYYYYYFYGMDVWGQGTTTVSS			SEQ ID NO:44	
VH1-8	(99)	-----			SEQ ID NO:1	
Consensus	(103)					

**Figure 38B**

	Section 1					
	1	10	20	30	40	52
CR2-1.49.1_LC	(1)	DIVMTQSPLSLEVTPGEPASISCRSBOSILLHNSNGNYLDWYLREGQSPQLL				
A19	(1)	DIVMTQSPLSLEVTPGEPASISCRSSQ8ILLHNSNGNYLDWYLQPGQSPQLL				
Consensus	(1)	DIVMTQSPLSLEVTPGEPASISCRSSQ8ILLHNSNGNYLDWYL KPGQSPQLL				
	Section 2					
	53	60	70	80	90	104
CR2-1.49.1_LC	(53)	IYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMOTLQITFGQ				
A19	(53)	IYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMOTLQITFGQ				
Consensus	(53)	IYLGS RASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQ LQT				
	Section 3					
	105	105	111			
CR2-1.49.1_LC	(105)	GTRLEIK			SEQ ID NO:45	
A19	(101)	-----			SEQ ID NO:8	
Consensus	(105)					



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**FIGURE 39**

**Figure 39A**

	Section 1					
	(1) 1	10	20	30	40	51
CR2-1.51.1 HC	(1) EVQLVQSGAEVKKPGESI	KI	SCKGSGYSGFTSYWIGWVR	VROMPGKGLEWMGII		
VH5-51	(1) EVQLVQSGAEVKKPGESI	KI	SCKGSGYSGFTSYWIGWVR	VROMPGKGLEWMGII		
Consensus	(1) EVQLVQSGAEVKKPGESI	KI	SCKGSGYSGFTSYWIGWVR	VROMPGKGLEWMGII		
	Section 2					
	(52) 52	60	70	80	90	102
CR2-1.51.1 HC	(52) YPGDSDA	Y9B3FQGQVTI	SADKS1	STAYLQWSSLKASDTAMYYCARHYDY		
VH5-51	(52) YPGDSDT	Y9B3FQGQVTI	SADKS1	STAYDQWSSLKASTAMYYCAR---		
Consensus	(52) YPGDSD	KY9PSFQGQVTI	SADKS1	STAYLQWSSLKASDTAMYYCAR		
	Section 3					
	(103) 103	110	126			
CR2-1.51.1 HC	(103) VWRNYRYTGWFDPWGQGTLTVSS			SEQ ID NO:46		
VH5-51	(99) -----			SEQ ID NO:6		
Consensus	(103)					

**Figure 39B**

	Section 1					
	(1) 1	10	20	30	40	52
CR2-1.51.1, LC	(1) EIVLTQSPGTLSLSPGERATLSCR	AQSVSSSYLAWYQQKEGQAPRLLIYGA				
A27	(1) EIVLTQSPGTLSLSPGERATLSCR	AQSVSSSYLAWYQQKEGQAPRLLIYGA				
Consensus	(1) EIVLTQSPGTLSLSPGERATLSCR	AQSVSSSYLAWYQQKEGQAPRLLIYGA				
	Section 2					
	(53) 53	60	70	80	90	104
CR2-1.51.1, LC	(53) SNNATGIPDRFSGSGSGTLP	LTLTISRLPEPDAVYYCQQYGS	SLPTFGPGTK			
A27	(53) SNNATGIPDRFSGSGSGTLP	LTLTISRLPEPDAVYYCQQYGS	SLPTFGPGTK			
Consensus	(53) S RATGIPDRFSGSGSGTLP	LTLTISRLPEPDAVYYCQQYGS	SLPTFGPGTK			
	Section 3					
	(105) 10508					
CR2-1.51.1, LC	(105) VDIK		SEQ ID NO:47			
A27	(97) -----		SEQ ID NO:10			
Consensus	(105)					



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**FIGURE 40**

Figure 40A

Figure 40B